

AU 1814
NOT Entered

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: WALLACH, DAVID
NOPHAR, YARON
KEMPER, OLIVER
ENGELMANN, HARTMUT
BRAKEBUSCH, CORD
ADERKA, DAN

See p. 7

(ii) TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
NECROSIS FACTOR BINDING PROTEIN I (TBP-I)

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

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(B) STREET: 419 Seventh Street, N.W., Suite 300
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20004

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/625668
(B) FILING DATE: 13-DEC-1990
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 25,618
(C) REFERENCE/DOCKET NUMBER: WALLACH4

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

Raw Sequence Listing
Patent Application US/07/625,66803/17/92
10:13:34

54 (D) TOPOLOGY: linear
55
56 (ii) MOLECULE TYPE: cDNA
57
58
59 (ix) FEATURE:
60 (A) NAME/KEY: CDS
61 (B) LOCATION: 256..1620
62
63 (ix) FEATURE:
64 (A) NAME/KEY: mat_peptide
65 (B) LOCATION: 319..1620
66
67
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
69
70 CGGCCCAGTG ATCTTGAACC CCAAAGGCCA GAACTGGAGC CTCAGTCCAG AGAATTCTGA 60
71
72 GAAAATTAAA GCAGAGAGGA GGGGAGAGAT CACTGGGACC AGGCCGTGAT CTCTATGCCC 120
73
74 GAGTCTCAAC CCTCAACTGT CACCCCAAGG CACTTGGGAC GTCCTGGACA GACCGAGTCC 180
75
76 CGGGAAGCCC CAGCACTGCC GCTGCCACAC TGCCCTGAGC CCAAATGGGG GAGTGAGAGG 240
77
78 CCATAGCTGT CTGGC ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCG 291
79 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro
80 -21 -20 -15 -10
81
82 CTG GTG CTC CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT 339
83 Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile
84 -5 1 5
85
86 GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT 387
87 Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys
88 10 15 20
89
90 CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC 435
91 Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
92 25 30 35
93
94 AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG 483
95 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly
96 40 45 50 55
97
98 CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA 531
99 Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser
100 60 65 70
101
102 GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC CGA AAG GAA 579
103 Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu
104 75 80 85
105
106 ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC CGG GAC ACC GTG 627

Patent Application US/07/625,668

107	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	
108			90					95					100				
109																	
110	TGT	GGC	TGC	AGG	AAG	AAC	CAG	TAC	CGG	CAT	TAT	TGG	AGT	GAA	AAC	CTT	675
111	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	
112		105					110					115					
113																	
114	TTC	CAG	TGC	TTC	AAT	TGC	AGC	CTC	TGC	CTC	AAT	GGG	ACC	GTG	CAC	CTC	723
115	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	
116	120					125					130					135	
117																	
118	TCC	TGC	CAG	GAG	AAA	CAG	AAC	ACC	GTG	TGC	ACC	TGC	CAT	GCA	GGT	TTC	771
119	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	
120					140					145					150		
121																	
122	TTT	CTA	AGA	GAA	AAC	GAG	TGT	GTC	TCC	TGT	AGT	AAC	TGT	AAG	AAA	AGC	819
123	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	
124				155					160					165			
125																	
126	CTG	GAG	TGC	ACG	AAG	TTG	TGC	CTA	CCC	CAG	ATT	GAG	AAT	GTT	AAG	GGC	867
127	Leu	Glu	Cys	Thr	Lys	Leu	Cys	Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	
128			170					175					180				
129																	
130	ACT	GAG	GAC	TCA	GGC	ACC	ACA	GTG	CTG	TTG	CCC	CTG	GTC	ATT	TTC	TTT	915
131	Thr	Glu	Asp	Ser	Gly	Thr	Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	
132		185					190					195					
133																	
134	GGT	CTT	TGC	CTT	TTA	TCC	CTC	CTC	TTC	ATT	GGT	TTA	ATG	TAT	CGC	TAC	963
135	Gly	Leu	Cys	Leu	Leu	Ser	Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	
136	200					205					210					215	
137																	
138	CAA	CGG	TGG	AAG	TCC	AAG	CTC	TAC	TCC	ATT	GTT	TGT	GGG	AAA	TCG	ACA	1011
139	Gln	Arg	Trp	Lys	Ser	Lys	Leu	Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	
140					220					225					230		
141																	
142	CCT	GAA	AAA	GAG	GGG	GAG	CTT	GAA	GGA	ACT	ACT	ACT	AAG	CCC	CTG	GCC	1059
143	Pro	Glu	Lys	Glu	Gly	Glu	Leu	Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	
144				235					240					245			
145																	
146	CCA	AAC	CCA	AGC	TTC	AGT	CCC	ACT	CCA	GGC	TTC	ACC	CCC	ACC	CTG	GGC	1107
147	Pro	Asn	Pro	Ser	Phe	Ser	Pro	Thr	Pro	Gly	Phe	Thr	Pro	Thr	Leu	Gly	
148			250					255					260				
149																	
150	TTC	AGT	CCC	GTG	CCC	AGT	TCC	ACC	TTC	ACC	TCC	AGC	TCC	ACC	TAT	ACC	1155
151	Phe	Ser	Pro	Val	Pro	Ser	Ser	Thr	Phe	Thr	Ser	Ser	Ser	Thr	Tyr	Thr	
152		265					270					275					
153																	
154	CCC	GGT	GAC	TGT	CCC	AAC	TTT	GCG	GCT	CCC	CGC	AGA	GAG	GTG	GCA	CCA	1203
155	Pro	Gly	Asp	Cys	Pro	Asn	Phe	Ala	Ala	Pro	Arg	Arg	Glu	Val	Ala	Pro	
156	280					285					290					295	
157																	
158	CCC	TAT	CAG	GGG	GCT	GAC	CCC	ATC	CTT	GCG	ACA	GCC	CTC	GCC	TCC	GAC	1251
159	Pro	Tyr	Gln	Gly	Ala	Asp	Pro	Ile	Leu	Ala	Thr	Ala	Leu	Ala	Ser	Asp	

Patent Application US/07/625,668

	300	305	310	
160				
161				
162	CCC ATC CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC CAC AAG CCA			1299
163	Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro			
164	315	320	325	
165				
166	CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC GCC GTG GTG GAG			1347
167	Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu			
168	330	335	340	
169				
170	AAC GTG CCC CCG TTG CGC TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG			1395
171	Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu			
172	345	350	355	
173				
174	AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG CAG AAC GGG CGC TGC CTG			1443
175	Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu			
176	360	365	370	375
177				
178	CGC GAG GCG CAA TAC AGC ATG CTG GCG ACC TGG AGG CGG CGC ACG CCG			1491
179	Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro			
180	380	385	390	
181				
182	CGG CGC GAG GCC ACG CTG GAG CTG CTG GGA CGC GTG CTC CGC GAC ATG			1539
183	Arg Arg Glu Ala Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met			
184	395	400	405	
185				
186	GAC CTG CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG CTT TGC GGC CCC			1587
187	Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro			
188	410	415	420	
189				
190	GCC GCC CTC CCG CCC GCG CCC AGT CTT CTC AGA TGAGGCTGCG CCCTGCGGGC			1640
191	Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg			
192	425	430		
193				
194	AGCTCTAAGG ACCGTCCTGC GAGATCGCCT TCCAACCCCA CTTTTTCTG GAAAGGAGGG			1700
195				
196	GTCTGTCAGG GGCAAGCAGG AGCTAGCAGC CGCTACTTG GTGCTAACCC CTCGATGTAC			1760
197				
198	ATAGCTTTTC TCAGCTGCCT GCGCGCCGCC GACAGTCAGC GCTGTGCGCG CGGAGAGAGG			1820
199				
200	TGCGCCGTGG GCTCAAGAGC CTGAGTGGGT GGTTTGCGAG GATGAGGGAC GCTATGCCTC			1880
201				
202	ATGCCCCGTTT TGGGTGTCCT CACCAGCAAG GCTGCTCGGG GGCCCCCTGGT TCGTCCCTGA			1940
203				
204	GCCTTTTTCA CAGTGCATAA GCAGTTTTTT TTGTTTTTGT TTTGTTTTGT TTTGTTTTTA			2000
205				
206	AATCAATCAT GTTACACTAA TAGAACTTG GCACTCCTGT GCCCTCTGCC TGGACAAGCA			2060
207				
208	CATAGCAAGC TGAAGTGTCC TAAGGCAGGG GCGAGCACGG AACAAATGGGG CCTTCAGCTG			2120
209				
210	GAGCTGTGGA CTTTTGTACA TACACTAAAA TTCTGAAGTT AAAAAAAAAA AAAAA			2175
211				
212				

Patent Application US/07/625,668

213 (2) INFORMATION FOR SEQ ID NO:2:

214

215 (i) SEQUENCE CHARACTERISTICS:

216 (A) LENGTH: 455 amino acids

217 (B) TYPE: amino acid

218 (D) TOPOLOGY: linear

219

220 (ii) MOLECULE TYPE: protein

221

222 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

223

224 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu

225 -21 -20 -15 -10

226

227 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro

228 -5 1 5 10

229

230 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys

231 15 20 25

232

233 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys

234 30 35 40

235

236 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp

237 45 50 55

238

239 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu

240 60 65 70 75

241

242 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val

243 80 85 90

244

245 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg

246 95 100 105

247

248 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe

249 110 115 120

250

251 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu

252 125 130 135

253

254 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu

255 140 145 150 155

256

257 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr

258 160 165 170

259

260 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser

261 175 180 185

262

263 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu

264 190 195 200

265

Patent Application US/07/625,668

266 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
267 205 210 215
268
269 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
270 220 225 230 235
271
272 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
273 240 245 250
274
275 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
276 255 260 265
277
278 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
279 270 275 280
280
281 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
282 285 290 295
283
284 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
285 300 305 310 315
286
287 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
288 320 325 330
289
290 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
291 335 340 345
292
293 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
294 350 355 360
295
296 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
297 365 370 375
298
299 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
300 380 385 390 395
301
302 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
303 400 405 410
304
305 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
306 415 420 425
307
308 Pro Ala Pro Ser Leu Leu Arg
309 430
310

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

319 (ii) MOLECULE TYPE: protein

320

321

322

323 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

324

325 GGIGTYCCIT TYATRTARGT DGGIGT "I" is not a valid 26
326 nucleic acid according
327 (2) INFORMATION FOR SEQ ID NO:4: to §1.822(b).
328

329 (i) SEQUENCE CHARACTERISTICS:

330 (A) LENGTH: 17 base pairs

331 (B) TYPE: nucleic acid

332 (C) STRANDEDNESS: single

333 (D) TOPOLOGY: linear

334

335 (ii) MOLECULE TYPE: cDNA

336

337

338

339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

340

341 GGNGTYCCNT TYATRTA

17

342

343 (2) INFORMATION FOR SEQ ID NO:5:

344

345 (i) SEQUENCE CHARACTERISTICS:

346 (A) LENGTH: 17 base pairs

347 (B) TYPE: nucleic acid

348 (C) STRANDEDNESS: single

349 (D) TOPOLOGY: linear

350

351 (ii) MOLECULE TYPE: cDNA

352

353

354

355 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

356

357 TTYATRTARG TDGGNGT

17

358

359 (2) INFORMATION FOR SEQ ID NO:6:

360

361 (i) SEQUENCE CHARACTERISTICS:

362 (A) LENGTH: 27 base pairs

363 (B) TYPE: nucleic acid

364 (C) STRANDEDNESS: single

365 (D) TOPOLOGY: linear

366

367 (ii) MOLECULE TYPE: cDNA

368

369

370

371 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

372
373 CGGCCGATGG GCCTCTCCAC CGTGCCT 27
374
375 (2) INFORMATION FOR SEQ ID NO:7:
376
377 (i) SEQUENCE CHARACTERISTICS:
378 (A) LENGTH: 27 base pairs
379 (B) TYPE: nucleic acid
380 (C) STRANDEDNESS: single
381 (D) TOPOLOGY: linear
382
383 (ii) MOLECULE TYPE: cDNA
384
385
386
387 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
388
389 AATAGTATTT CTAATCTGGG GTAGGCA 27
390
391 (2) INFORMATION FOR SEQ ID NO:8:
392
393 (i) SEQUENCE CHARACTERISTICS:
394 (A) LENGTH: 6 amino acids
395 (B) TYPE: amino acid
396 (C) STRANDEDNESS: single
397 (D) TOPOLOGY: linear
398
399 (ii) MOLECULE TYPE: peptide
400
401
402
403 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
404
405 Met Asp Ser Val Cys Pro
406 1 5
407
408 (2) INFORMATION FOR SEQ ID NO:9:
409
410 (i) SEQUENCE CHARACTERISTICS:
411 (A) LENGTH: 23 base pairs
412 (B) TYPE: nucleic acid
413 (C) STRANDEDNESS: single
414 (D) TOPOLOGY: linear
415
416 (ii) MOLECULE TYPE: cDNA
417
418
419
420 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
421
422 AATTCATGGA TAGTGTGTGT CCC 23
423
424 (2) INFORMATION FOR SEQ ID NO:10:

425
426 (i) SEQUENCE CHARACTERISTICS:
427 (A) LENGTH: 23 base pairs
428 (B) TYPE: nucleic acid
429 (C) STRANDEDNESS: single
430 (D) TOPOLOGY: linear
431
432 (ii) MOLECULE TYPE: cDNA
433
434
435
436 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
437
438 GTACCTATCA CACACAGGGG TTC 23
439
440 (2) INFORMATION FOR SEQ ID NO:11:
441
442 (i) SEQUENCE CHARACTERISTICS:
443 (A) LENGTH: 22 amino acids
444 (B) TYPE: amino acid
445 (C) STRANDEDNESS: single
446 (D) TOPOLOGY: linear
447
448 (ii) MOLECULE TYPE: peptide
449
450
451
452 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
453
454 Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
455 1 5 10 15
456
457 Arg Leu Arg Glu Tyr Tyr
458 20
459
460 (2) INFORMATION FOR SEQ ID NO:12:
461
462 (i) SEQUENCE CHARACTERISTICS:
463 (A) LENGTH: 7 amino acids
464 (B) TYPE: amino acid
465 (C) STRANDEDNESS: single
466 (D) TOPOLOGY: linear
467
468 (ii) MOLECULE TYPE: cDNA
469
470
471
472 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
473
474 Leu Cys Ala Pro Leu Arg Lys
475 1 5
476
477 (2) INFORMATION FOR SEQ ID NO:13:

478
479 (i) SEQUENCE CHARACTERISTICS:
480 (A) LENGTH: 9 amino acids
481 (B) TYPE: amino acid
482 (C) STRANDEDNESS: single
483 (D) TOPOLOGY: linear
484
485 (ii) MOLECULE TYPE: peptide
486
487
488
489 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
490
491 Cys Arg Pro Gly Phe Gly Val Ala Arg
492 1 5
493
494 (2) INFORMATION FOR SEQ ID NO:14:
495
496 (i) SEQUENCE CHARACTERISTICS:
497 (A) LENGTH: 11 amino acids
498 (B) TYPE: amino acid
499 (C) STRANDEDNESS: single
500 (D) TOPOLOGY: linear
501
502 (ii) MOLECULE TYPE: peptide
503
504
505
506 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
507
508 Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
509 1 5 10
510
511 (2) INFORMATION FOR SEQ ID NO:15:
512
513 (i) SEQUENCE CHARACTERISTICS:
514 (A) LENGTH: 12 amino acids
515 (B) TYPE: amino acid
516 (C) STRANDEDNESS: single
517 (D) TOPOLOGY: linear
518
519 (ii) MOLECULE TYPE: peptide
520
521
522
523 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
524
525 Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser
526 1 5 10
527
528 (2) INFORMATION FOR SEQ ID NO:16:
529
530 (i) SEQUENCE CHARACTERISTICS:

531 (A) LENGTH: 8 amino acids
532 (B) TYPE: amino acid
533 (C) STRANDEDNESS: single
534 (D) TOPOLOGY: linear
535
536 (ii) MOLECULE TYPE: peptide
537
538
539
540 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
541
542 Ser Cys Gly Pro Ser Tyr Pro Asp
543 1 5
544
545 (2) INFORMATION FOR SEQ ID NO:17:
546
547 (i) SEQUENCE CHARACTERISTICS:
548 (A) LENGTH: 13 amino acids
549 (B) TYPE: amino acid
550 (C) STRANDEDNESS: single
551 (D) TOPOLOGY: linear
552
553 (ii) MOLECULE TYPE: peptide
554
555
556
557 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
558
559 Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg
560 1 5 10
561
562 (2) INFORMATION FOR SEQ ID NO:18:
563
564 (i) SEQUENCE CHARACTERISTICS:
565 (A) LENGTH: 13 amino acids
566 (B) TYPE: amino acid
567 (C) STRANDEDNESS: single
568 (D) TOPOLOGY: linear
569
570 (ii) MOLECULE TYPE: peptide
571
572
573
574 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
575
576 Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
577 1 5 10
578
579 (2) INFORMATION FOR SEQ ID NO:19:
580
581 (i) SEQUENCE CHARACTERISTICS:
582 (A) LENGTH: 9 amino acids
583 (B) TYPE: amino acid

Patent Application US/07/625,668

584 (C) STRANDEDNESS: single
585 (D) TOPOLOGY: linear
586
587 (ii) MOLECULE TYPE: peptide
588
589
590
591 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
592
593 Pro Gly Trp Tyr Cys Ala Leu Ser Lys
594 1 5
595
596 (2) INFORMATION FOR SEQ ID NO:20:
597
598 (i) SEQUENCE CHARACTERISTICS:
599 (A) LENGTH: 17 amino acids
600 (B) TYPE: amino acid
601 (C) STRANDEDNESS: single
602 (D) TOPOLOGY: linear
603
604 (ii) MOLECULE TYPE: peptide
605
606
607
608 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
609
610 Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
611 1 5 10 15
612
613 Arg
614
615
616 (2) INFORMATION FOR SEQ ID NO:21:
617
618 (i) SEQUENCE CHARACTERISTICS:
619 (A) LENGTH: 15 amino acids
620 (B) TYPE: amino acid
621 (C) STRANDEDNESS: single
622 (D) TOPOLOGY: linear
623
624 (ii) MOLECULE TYPE: peptide
625
626
627
628 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
629
630 Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg
631 1 5 10 15
632
633 (2) INFORMATION FOR SEQ ID NO:22:
634
635 (i) SEQUENCE CHARACTERISTICS:
636 (A) LENGTH: 9 amino acids

637 (B) TYPE: amino acid
638 (C) STRANDEDNESS: single
639 (D) TOPOLOGY: linear
640
641 (ii) MOLECULE TYPE: peptide
642
643
644
645 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
646
647 Cys Arg Pro Gly Phe Gly Val Ala Arg
648 1 5
649
650 (2) INFORMATION FOR SEQ ID NO:23:
651
652 (i) SEQUENCE CHARACTERISTICS:
653 (A) LENGTH: 13 amino acids
654 (B) TYPE: amino acid
655 (C) STRANDEDNESS: single
656 (D) TOPOLOGY: linear
657
658 (ii) MOLECULE TYPE: peptide
659
660
661
662 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
663
664 Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser
665 1 5 10
666
667 (2) INFORMATION FOR SEQ ID NO:24:
668
669 (i) SEQUENCE CHARACTERISTICS:
670 (A) LENGTH: 20 amino acids
671 (B) TYPE: amino acid
672 (C) STRANDEDNESS: single
673 (D) TOPOLOGY: linear
674
675 (ii) MOLECULE TYPE: peptide
676
677
678
679 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
680
681 Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly
682 1 5 10 15
683
684 Thr Phe Ser Lys
685 20
686
687 (2) INFORMATION FOR SEQ ID NO:25:
688
689 (i) SEQUENCE CHARACTERISTICS:

690 (A) LENGTH: 20 amino acids
691 (B) TYPE: amino acid
692 (C) STRANDEDNESS: single
693 (D) TOPOLOGY: linear
694
695 (ii) MOLECULE TYPE: peptide
696
697
698
699 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
700
701 Cys Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp
702 1 5 10 15
703
704 Val Val Cys Lys
705 20
706
707 (2) INFORMATION FOR SEQ ID NO:26:
708
709 (i) SEQUENCE CHARACTERISTICS:
710 (A) LENGTH: 18 amino acids
711 (B) TYPE: amino acid
712 (C) STRANDEDNESS: single
713 (D) TOPOLOGY: linear
714
715 (ii) MOLECULE TYPE: peptide
716
717
718
719 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
720
721 Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln
722 1 5 10 15
723
724 Leu Trp
725

LINE ERROR

ORIGINAL TEXT

33 Wrong application Serial Number
325 Wrong Nucleic Acid Designator
323 Entered and Calc. Seq. Length differ

(A) APPLICATION NUMBER: US 07/625668
GGIGTYCCIT TYATRTARGET DGGIGT
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

LINE ORIGINAL TEXT

CORRECTED TEXT